

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 17, 2004, 06:49:42 ; Search time 2636.98 Seconds
(without alignments)
2842.425 Million cell updates/sec

Title: US-08-737-319-1
Perfect score: 1341
Sequence: 1 MSMPNIVPPAEVRTEGLSLE.....KGEVDAKSLEDLSDNKVWKM 251

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US08737319/runat_15042004_131641_26714/app_query.fasta_1.8
46

-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US08737319_@CGN_1_1_2463_@runat_15042004_131641_26714 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*

11: gb_htc:*
 12: gb_est3:*
 13: gb_est4:*
 14: gb_est5:*
 15: em_estfun:*
 16: em_estom:*
 17: em_gss_hum:*
 18: em_gss_inv:*
 19: em_gss_pln:*
 20: em_gss_vrt:*
 21: em_gss_fun:*
 22: em_gss_mam:*
 23: em_gss_mus:*
 24: em_gss_pro:*
 25: em_gss_rod:*
 26: em_gss_phg:*
 27: em_gss_vrl:*
 28: gb_gssl:*
 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				Description
	No.	Score	Match	Length	DB	ID	
c	1	643	47.9	1051	29	CNS076H2	AL431388 T3 end of
	2	636	47.4	969	14	CD456156	CD456156 Fg03_08f1
	3	597	44.5	777	13	BX853590	BX853590 BX853590
	4	594.5	44.3	729	13	BX867082	BX867082 BX867082
	5	591.5	44.1	1051	14	CD507557	CD507557 CDA85-H04
	6	591.5	44.1	1219	14	CD497570	CD497570 CDA28-F04
	7	590.5	44.0	1111	14	CK231818	CK231818 ILLUMIGEN
	8	588.5	43.9	864	13	BX721162	BX721162 BX721162
	9	588.5	43.9	881	13	BX743804	BX743804 BX743804
	10	588.5	43.9	890	13	BX718091	BX718091 BX718091
	11	585	43.6	762	14	CF869867	CF869867 tric020xl
	12	585	43.6	817	14	CB900020	CB900020 tric020xl
	13	584.5	43.6	711	14	CF524263	CF524263 AGENCOURT
	14	582	43.4	753	14	CF873428	CF873428 tric033xc
	15	582	43.4	824	14	CB903168	CB903168 tric033xc
c	16	580	43.3	646	14	CB059459	CB059459 4008699 B
	17	579.5	43.2	687	29	AY412293	AY412293 Homo sapi
	18	579.5	43.2	838	13	BU177117	BU177117 AGENCOURT
	19	579.5	43.2	857	13	BQ225771	BQ225771 AGENCOURT
	20	579.5	43.2	1032	9	AL545986	AL545986 AL545986
	21	579.5	43.2	1150	9	AL551638	AL551638 AL551638
	22	579.5	43.2	1201	9	AL557778	AL557778 AL557778
	23	579.5	43.2	1201	9	AL558036	AL558036 AL558036
	24	579	43.2	988	14	CF883213	CF883213 tric033xc
	25	579	43.2	1002	12	BM452536	BM452536 AGENCOURT
	26	577	43.0	862	13	BQ227719	BQ227719 AGENCOURT
	27	574.5	42.8	1201	9	AL513826	AL513826 AL513826
	28	574	42.8	813	13	BU287141	BU287141 603607694

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 17, 2004, 06:49:40 ; Search time 73.3314 Seconds
(without alignments)
1899.496 Million cell updates/sec

Title: US-08-737-319-1
Perfect score: 1341
Sequence: 1 MSMPNIVPPAEVRTEGLSLE.....KGEVDAKSLEDLSDNKVWKM 251

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US08737319/runat_15042004_131642_26729/app_query.fasta_1.8
46

-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US08737319@CGN_1_1_76@runat_15042004_131642_26729 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

USPA 63 2941

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1341	100.0	1165	4	US-09-091-725-20	Sequence 20, Appl
2	552	41.2	1270	4	US-09-323-998E-29	Sequence 29, Appl
3	547	40.8	1002	4	US-09-323-998E-28	Sequence 28, Appl
4	541	40.3	1031	4	US-09-323-998E-35	Sequence 35, Appl
5	534.5	39.9	996	1	US-08-624-125-10	Sequence 10, Appl
6	534.5	39.9	996	4	US-08-937-155-10	Sequence 10, Appl
7	534.5	39.9	996	4	US-09-323-998E-10	Sequence 10, Appl
8	529.5	39.5	988	4	US-09-323-998E-32	Sequence 32, Appl
9	527	39.3	954	1	US-08-624-125-9	Sequence 9, Appli
10	527	39.3	954	4	US-08-937-155-9	Sequence 9, Appli
11	527	39.3	954	4	US-09-323-998E-9	Sequence 9, Appli
12	520.5	38.8	985	4	US-09-323-998E-31	Sequence 31, Appl
13	516.5	38.5	956	4	US-09-323-998E-34	Sequence 34, Appl
14	513.5	38.3	1288	4	US-09-296-754-1	Sequence 1, Appli
15	510	38.0	1020	3	US-09-201-641-7	Sequence 7, Appli
16	500	37.3	1874	4	US-09-323-998E-33	Sequence 33, Appl
17	498	37.1	1109	4	US-09-323-998E-30	Sequence 30, Appl
18	493	36.8	1165	1	US-08-624-125-11	Sequence 11, Appl
19	493	36.8	1165	4	US-08-937-155-11	Sequence 11, Appl
20	493	36.8	1165	4	US-09-323-998E-11	Sequence 11, Appl
21	490	36.5	1135	1	US-08-624-125-12	Sequence 12, Appl
22	490	36.5	1135	4	US-08-937-155-12	Sequence 12, Appl
23	490	36.5	1135	4	US-09-323-998E-12	Sequence 12, Appl
24	242	18.0	390	4	US-09-621-976-2553	Sequence 2553, Ap
25	220.5	16.4	960	1	US-08-624-125-13	Sequence 13, Appl
26	220.5	16.4	960	4	US-08-937-155-13	Sequence 13, Appl
27	220.5	16.4	960	4	US-09-323-998E-13	Sequence 13, Appl
28	210.5	15.7	567	4	US-09-543-681A-3136	Sequence 3136, Ap
29	175	13.0	600	4	US-09-489-039A-4697	Sequence 4697, Ap
c 30	159	11.9	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c 31	159	11.9	4411529	3	US-09-103-840A-1	Sequence 1, Appli
32	95.5	7.1	2034	4	US-09-328-352-239	Sequence 239, App
33	94.5	7.0	606	4	US-09-543-681A-129	Sequence 129, App
c 34	93.5	7.0	480	4	US-09-621-976-220	Sequence 220, App
c 35	90.5	6.7	1462	4	US-08-956-171E-771	Sequence 771, App
36	90.5	6.7	4215	4	US-09-657-452A-3	Sequence 3, Appli
37	90.5	6.7	22671	4	US-08-976-259-14	Sequence 14, Appl
38	89	6.6	612	4	US-09-252-991A-10562	Sequence 10562, A
c 39	89	6.6	2313	4	US-09-252-991A-10294	Sequence 10294, A
40	88.5	6.6	561	4	US-09-489-039A-5425	Sequence 5425, Ap
c 41	88.5	6.6	1230	3	US-09-188-930-25	Sequence 25, Appl
c 42	88.5	6.6	1230	3	US-09-188-930-201	Sequence 201, App
c 43	88.5	6.6	1230	4	US-09-312-283C-25	Sequence 25, Appl
c 44	88.5	6.6	1230	4	US-09-312-283C-201	Sequence 201, App
45	87	6.5	19056	3	US-09-272-032-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-091-725-20

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 17, 2004, 06:49:40 ; Search time 414.888 Seconds
(without alignments)
2707.042 Million cell updates/sec

Title: US-08-737-319-1
Perfect score: 1341
Sequence: 1 MSMPNIVPPAEVRTEGLSLE.....KGEVDAKSLEDLSDNKVWKM 251

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 2890132 seqs, 2237290429 residues

Total number of hits satisfying chosen parameters: 5780264

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US08737319/runat_15042004_131643_26809/app_query.fasta_1.8
46

-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US08737319_@CGN_1_1_71_@runat_15042004_131643_26809
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

```

11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	819	61.1	846	15	US-10-320-797-2065	Sequence 2065, Ap
2	695	51.8	1019	15	US-10-320-797-1065	Sequence 1065, Ap
3	695	51.8	3019	15	US-10-320-797-65	Sequence 65, Appl
4	640.5	47.8	816	14	US-10-128-714-2424	Sequence 2424, Ap
5	629	46.9	855	14	US-10-032-585-6474	Sequence 6474, Ap
6	627.5	46.8	816	14	US-10-128-714-7424	Sequence 7424, Ap
7	623	46.5	8400	10	US-09-918-740-64	Sequence 64, Appl
8	623	46.5	14623	10	US-09-918-740-74	Sequence 74, Appl
9	623	46.5	14623	10	US-09-918-740-76	Sequence 76, Appl
10	621	46.3	684	10	US-09-918-740-23	Sequence 23, Appl
11	621	46.3	684	10	US-09-918-740-54	Sequence 54, Appl
12	579.5	43.2	1807	9	US-09-880-107-3712	Sequence 3712, Ap
13	579.5	43.2	1920	12	US-10-363-616-20	Sequence 20, Appl
14	579.5	43.2	2059	10	US-09-814-353-20314	Sequence 20314, A
15	578.5	43.1	867	15	US-10-369-493-46169	Sequence 46169, A
16	560.5	41.8	1182	15	US-10-388-934-12	Sequence 12, Appl
17	552.5	41.2	2957	14	US-10-128-714-424	Sequence 424, App
18	552.5	41.2	2958	14	US-10-128-714-5424	Sequence 5424, Ap
19	552	41.2	1271	9	US-09-323-998D-29	Sequence 29, Appl
20	547	40.8	1002	9	US-09-323-998D-28	Sequence 28, Appl
21	546.5	40.8	958	14	US-10-128-714-1424	Sequence 1424, Ap
22	546.5	40.8	958	14	US-10-128-714-6424	Sequence 6424, Ap
23	541	40.3	1031	9	US-09-323-998D-35	Sequence 35, Appl
24	540	40.3	775	15	US-10-369-493-27183	Sequence 27183, A
25	536.5	40.0	807	15	US-10-369-493-26033	Sequence 26033, A
26	536.5	40.0	807	15	US-10-369-493-26038	Sequence 26038, A
27	534.5	39.9	996	9	US-09-323-998D-10	Sequence 10, Appl
28	530.5	39.6	855	9	US-09-938-842A-572	Sequence 572, App
29	530.5	39.6	855	11	US-09-938-842A-572	Sequence 572, App
30	530.5	39.6	880	14	US-10-342-224-95	Sequence 95, Appl
31	529.5	39.5	988	9	US-09-323-998D-32	Sequence 32, Appl
32	528.5	39.4	876	9	US-09-938-842A-292	Sequence 292, App
33	528.5	39.4	876	11	US-09-938-842A-292	Sequence 292, App
34	527	39.3	954	9	US-09-323-998D-9	Sequence 9, Appli
35	520.5	38.8	985	9	US-09-323-998D-31	Sequence 31, Appl
36	517.5	38.6	827	15	US-10-369-493-36552	Sequence 36552, A
37	501	37.4	954	9	US-09-323-998D-34	Sequence 34, Appl
38	500	37.3	1874	9	US-09-323-998D-33	Sequence 33, Appl
39	498	37.1	1109	9	US-09-323-998D-30	Sequence 30, Appl

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 17, 2004, 06:49:42 ; Search time 2721.02 Seconds
(without alignments)
2842.425 Million cell updates/sec

Title: US-08-737-319-2
Perfect score: 1398
Sequence: 1 MQLLAEDRTDHMRGASTWAG.....AALNTDKHEDWGTVHHINEA 259

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

-
Q=/cgn2_1/USPTO_spool/US08737319/runat_15042004_131641_26714/app_query.fasta_1.8
46

-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US08737319_CGN_1_1_2463_runat_15042004_131641_26714 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*

```

11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	542.5	38.8	969	14	CD456156	CD456156 Fg03_08f1
2	534.5	38.2	782	13	BQ802836	BQ802836 WHE2830_E
3	532	38.1	779	13	BU100364	BU100364 WHE3352_D
4	531	38.0	717	13	BQ483516	BQ483516 WHE3509_E
5	530.5	37.9	1168	14	CK171569	CK171569 FGAS04688
6	529	37.8	794	13	BQ806442	BQ806442 WHE3579_B
c 7	529	37.8	1051	29	CNS076H2	AL431388 T3 end of
8	527	37.7	748	12	BG600002	BG600002 EST504897
9	527	37.7	905	14	CK274547	CK274547 EST720625
10	527	37.7	949	14	CK268206	CK268206 EST714284
11	526	37.6	842	14	CF651376	CF651376 25-E00921
12	526	37.6	842	14	CF651377	CF651377 25-E02110
13	524	37.5	694	14	CB679092	CB679092 OSJNEf02C
14	522	37.3	852	12	BG418760	BG418760 HVSMEk002
15	521	37.3	685	12	BG097786	BG097786 EST462305
16	520	37.2	837	14	CD445983	CD445983 EL01T0206
17	520	37.2	861	14	CD438249	CD438249 EL01N0511
18	517	37.0	1155	14	CB329952	CB329952 SpEST1106
19	507	36.3	670	14	CA800263	CA800263 sau13c07.
20	503.5	36.0	1111	14	CK231818	CK231818 ILLUMIGEN
21	502.5	35.9	710	14	CB685009	CB685009 OSJNEf15B
22	502	35.9	1193	11	AY104380	AY104380 Zea mays
23	501	35.8	889	12	BM816948	BM816948 HB106H05_
24	499.5	35.7	720	14	CF233376	CF233376 PtaJXO002
25	498	35.6	700	12	BG600687	BG600687 EST505594
26	497.5	35.6	753	14	CF873428	CF873428 tric033xc
27	497.5	35.6	824	14	CB903168	CB903168 tric033xc
28	497	35.6	864	13	BX721162	BX721162 BX721162

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 17, 2004, 06:49:40 ; Search time 75.6686 Seconds
(without alignments)
1899.496 Million cell updates/sec

Title: US-08-737-319-2
Perfect score: 1398
Sequence: 1 MQLLAEDRTDHMRGASTWAG.....AALNTDKHEDWGTVHHINEA 259

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US08737319/runat_15042004_131642_26729/app_query.fasta_1.8
46

-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US08737319_@CGN_1_1_76_@runat_15042004_131642_26729 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1394	99.7	1109	4	US-09-323-998E-30	Sequence 30, Appl
2	1383	98.9	1135	1	US-08-624-125-12	Sequence 12, Appl
3	1383	98.9	1135	4	US-08-937-155-12	Sequence 12, Appl
4	1383	98.9	1135	4	US-09-323-998E-12	Sequence 12, Appl
5	1368	97.9	1165	1	US-08-624-125-11	Sequence 11, Appl
6	1368	97.9	1165	4	US-08-937-155-11	Sequence 11, Appl
7	1368	97.9	1165	4	US-09-323-998E-11	Sequence 11, Appl
8	777.5	55.6	1874	4	US-09-323-998E-33	Sequence 33, Appl
9	527	37.7	988	4	US-09-323-998E-32	Sequence 32, Appl
10	527	37.7	1031	4	US-09-323-998E-35	Sequence 35, Appl
11	523	37.4	1020	3	US-09-201-641-7	Sequence 7, Appli
12	522	37.3	996	1	US-08-624-125-10	Sequence 10, Appl
13	522	37.3	996	4	US-08-937-155-10	Sequence 10, Appl
14	522	37.3	996	4	US-09-323-998E-10	Sequence 10, Appl
15	521	37.3	954	1	US-08-624-125-9	Sequence 9, Appli
16	521	37.3	954	4	US-08-937-155-9	Sequence 9, Appli
17	521	37.3	954	4	US-09-323-998E-9	Sequence 9, Appli
18	517	37.0	1002	4	US-09-323-998E-28	Sequence 28, Appl
19	517	37.0	1288	4	US-09-296-754-1	Sequence 1, Appli
20	516	36.9	956	4	US-09-323-998E-34	Sequence 34, Appl
21	516	36.9	985	4	US-09-323-998E-31	Sequence 31, Appl
22	510	36.5	1270	4	US-09-323-998E-29	Sequence 29, Appl
23	494	35.3	1165	4	US-09-091-725-20	Sequence 20, Appl
24	263	18.8	960	1	US-08-624-125-13	Sequence 13, Appl
25	263	18.8	960	4	US-08-937-155-13	Sequence 13, Appl
26	263	18.8	960	4	US-09-323-998E-13	Sequence 13, Appl
27	254.5	18.2	567	4	US-09-543-681A-3136	Sequence 3136, Ap
28	210	15.0	390	4	US-09-621-976-2553	Sequence 2553, Ap
29	195	13.9	600	4	US-09-489-039A-4697	Sequence 4697, Ap
c 30	191.5	13.7	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c 31	191.5	13.7	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c 32	113.5	8.1	480	4	US-09-621-976-220	Sequence 220, App
33	107	7.7	612	4	US-09-252-991A-10562	Sequence 10562, A
c 34	107	7.7	2313	4	US-09-252-991A-10294	Sequence 10294, A
35	91.5	6.5	561	4	US-09-489-039A-5425	Sequence 5425, Ap
36	91.5	6.5	4403765	3	US-09-103-840A-2	Sequence 2, Appli
37	91.5	6.5	4411529	3	US-09-103-840A-1	Sequence 1, Appli
38	90.5	6.5	621	4	US-09-107-532A-1542	Sequence 1542, Ap
39	89.5	6.4	606	4	US-09-543-681A-129	Sequence 129, App
c 40	89	6.4	1272	4	US-09-252-991A-2090	Sequence 2090, Ap
c 41	86.5	6.2	2061	4	US-09-252-991A-3938	Sequence 3938, Ap
c 42	86.5	6.2	2316	4	US-09-252-991A-3884	Sequence 3884, Ap
43	86.5	6.2	2328	4	US-09-252-991A-3965	Sequence 3965, Ap
c 44	86.5	6.2	23673	4	US-09-773-816-1	Sequence 1, Appli
c 45	86	6.2	2933	4	US-08-936-165A-201	Sequence 201, App

Cunningham
family

6642021

US 664482

5744341

6524811

ALIGNMENTS

RESULT 1

US-09-323-998E-30

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 17, 2004, 06:49:40 ; Search time 428.112 Seconds
(without alignments)
2707.042 Million cell updates/sec

Title: US-08-737-319-2
Perfect score: 1398
Sequence: 1 MQLLAEDRTDHMRGASTWAG.....AALNTDKHEDWGTVHHINEA 259

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2890132 seqs, 2237290429 residues

Total number of hits satisfying chosen parameters: 5780264

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US08737319/runat_15042004_131643_26809/app_query.fasta_1.8
46

-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US08737319_@CGN_1_1_71_@runat_15042004_131643_26809
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

```

11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1394	99.7	1109	9	US-09-323-998D-30	Sequence 30, Appl
2	1383	98.9	1135	9	US-09-323-998D-12	Sequence 12, Appl
3	1368	97.9	1165	9	US-09-323-998D-11	Sequence 11, Appl
4	777.5	55.6	1874	9	US-09-323-998D-33	Sequence 33, Appl
5	538	38.5	816	14	US-10-128-714-2424	Sequence 2424, Ap
6	527	37.7	988	9	US-09-323-998D-32	Sequence 32, Appl
7	527	37.7	1031	9	US-09-323-998D-35	Sequence 35, Appl
8	526	37.6	816	14	US-10-128-714-7424	Sequence 7424, Ap
9	526	37.6	876	9	US-09-938-842A-292	Sequence 292, App
10	526	37.6	876	11	US-09-938-842A-292	Sequence 292, App
11	522	37.3	684	10	US-09-918-740-23	Sequence 23, Appl
12	522	37.3	684	10	US-09-918-740-54	Sequence 54, Appl
13	522	37.3	996	9	US-09-323-998D-10	Sequence 10, Appl
14	522	37.3	8400	10	US-09-918-740-64	Sequence 64, Appl
15	522	37.3	14623	10	US-09-918-740-74	Sequence 74, Appl
16	522	37.3	14623	10	US-09-918-740-76	Sequence 76, Appl
17	521	37.3	954	9	US-09-323-998D-9	Sequence 9, Appli
18	517	37.0	1002	9	US-09-323-998D-28	Sequence 28, Appl
19	516	36.9	985	9	US-09-323-998D-31	Sequence 31, Appl
20	515	36.8	855	9	US-09-938-842A-572	Sequence 572, App
21	515	36.8	855	11	US-09-938-842A-572	Sequence 572, App
22	515	36.8	880	14	US-10-342-224-95	Sequence 95, Appl
23	513	36.7	855	14	US-10-032-585-6474	Sequence 6474, Ap
24	510	36.5	1271	9	US-09-323-998D-29	Sequence 29, Appl
25	496	35.5	867	15	US-10-369-493-46169	Sequence 46169, A
26	495.5	35.4	954	9	US-09-323-998D-34	Sequence 34, Appl
27	495.5	35.4	1807	9	US-09-880-107-3712	Sequence 3712, Ap
28	495.5	35.4	1920	12	US-10-363-616-20	Sequence 20, Appl
29	495.5	35.4	2059	10	US-09-814-353-20314	Sequence 20314, A
30	488	34.9	846	15	US-10-320-797-2065	Sequence 2065, Ap
31	472	33.8	1182	15	US-10-388-934-12	Sequence 12, Appl
32	464.5	33.2	775	15	US-10-369-493-27183	Sequence 27183, A
33	464	33.2	958	14	US-10-128-714-1424	Sequence 1424, Ap
34	464	33.2	958	14	US-10-128-714-6424	Sequence 6424, Ap
35	464	33.2	2957	14	US-10-128-714-424	Sequence 424, App
36	464	33.2	2958	14	US-10-128-714-5424	Sequence 5424, Ap
37	456.5	32.7	807	15	US-10-369-493-26033	Sequence 26033, A
38	456.5	32.7	807	15	US-10-369-493-26038	Sequence 26038, A
39	449.5	32.2	827	15	US-10-369-493-36552	Sequence 36552, A